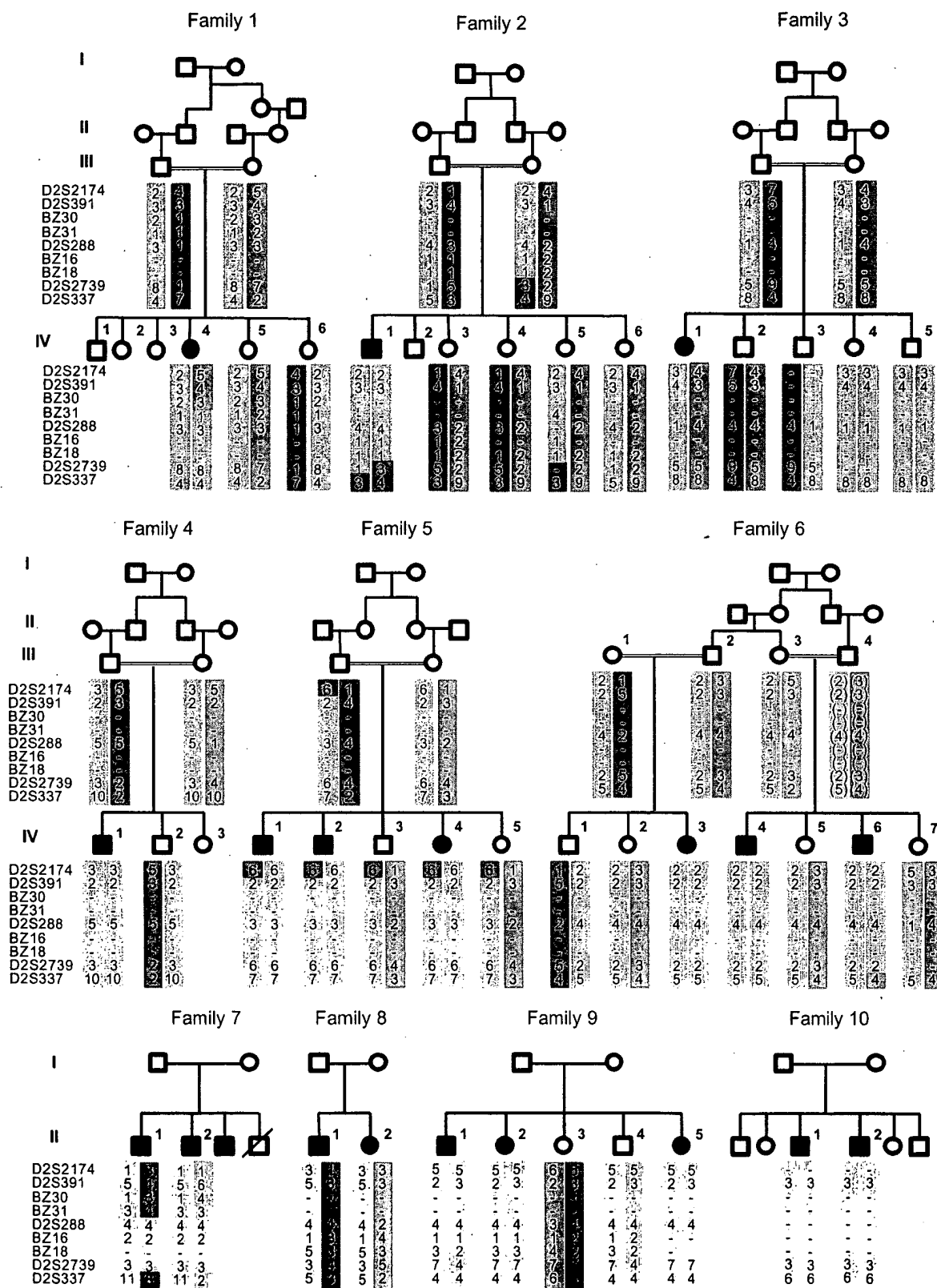


FIG 1



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FIG 2

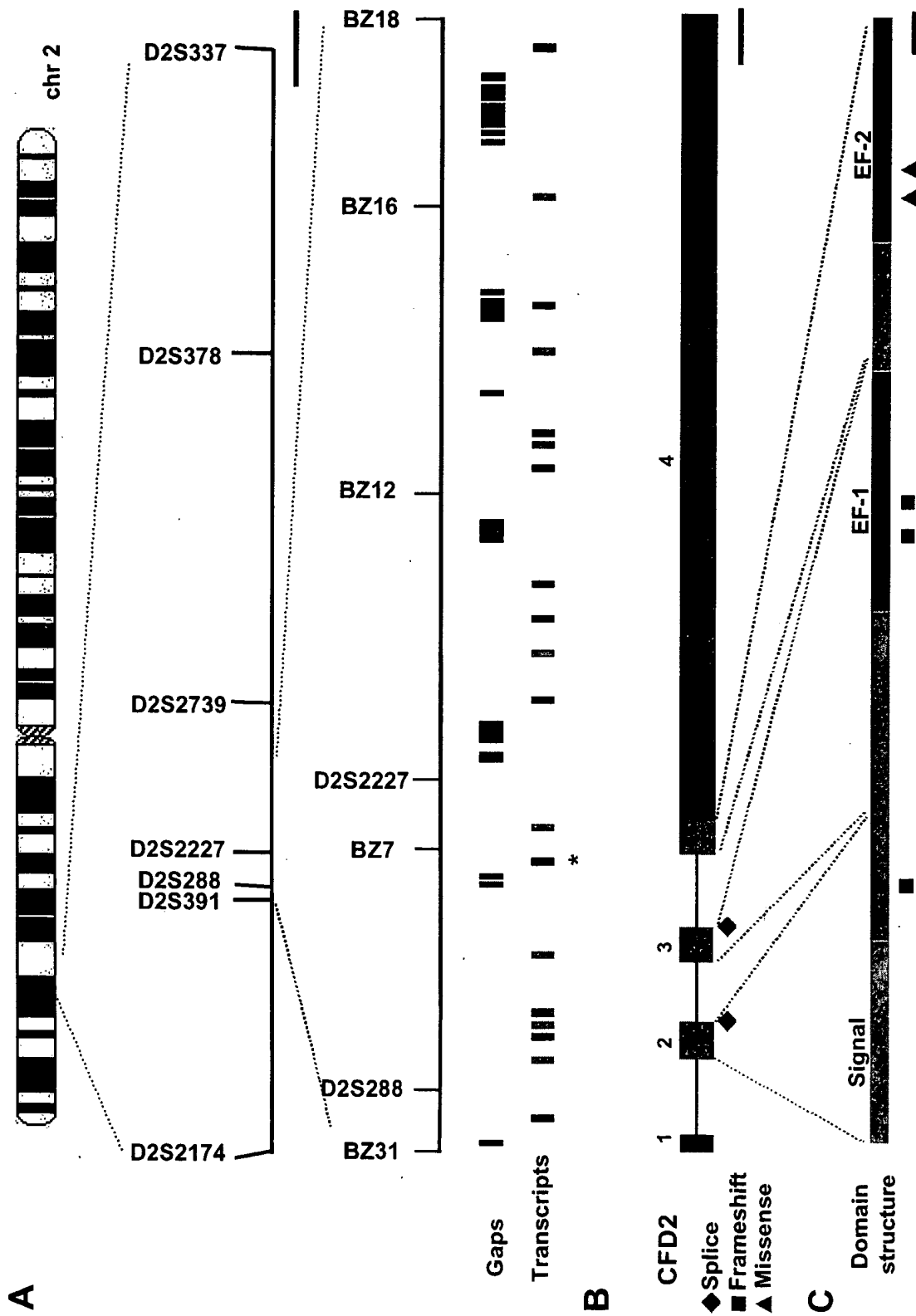
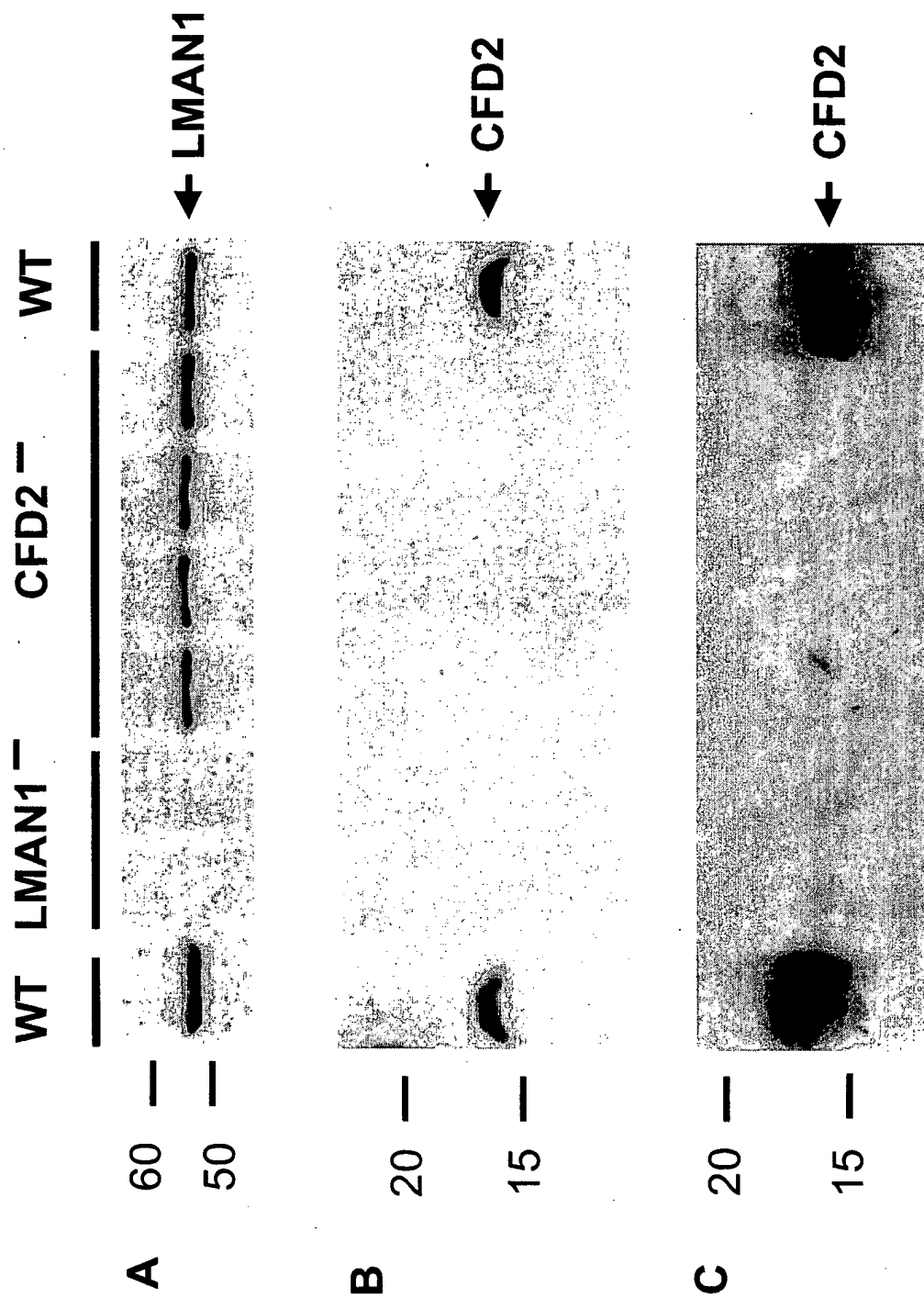


FIG 3



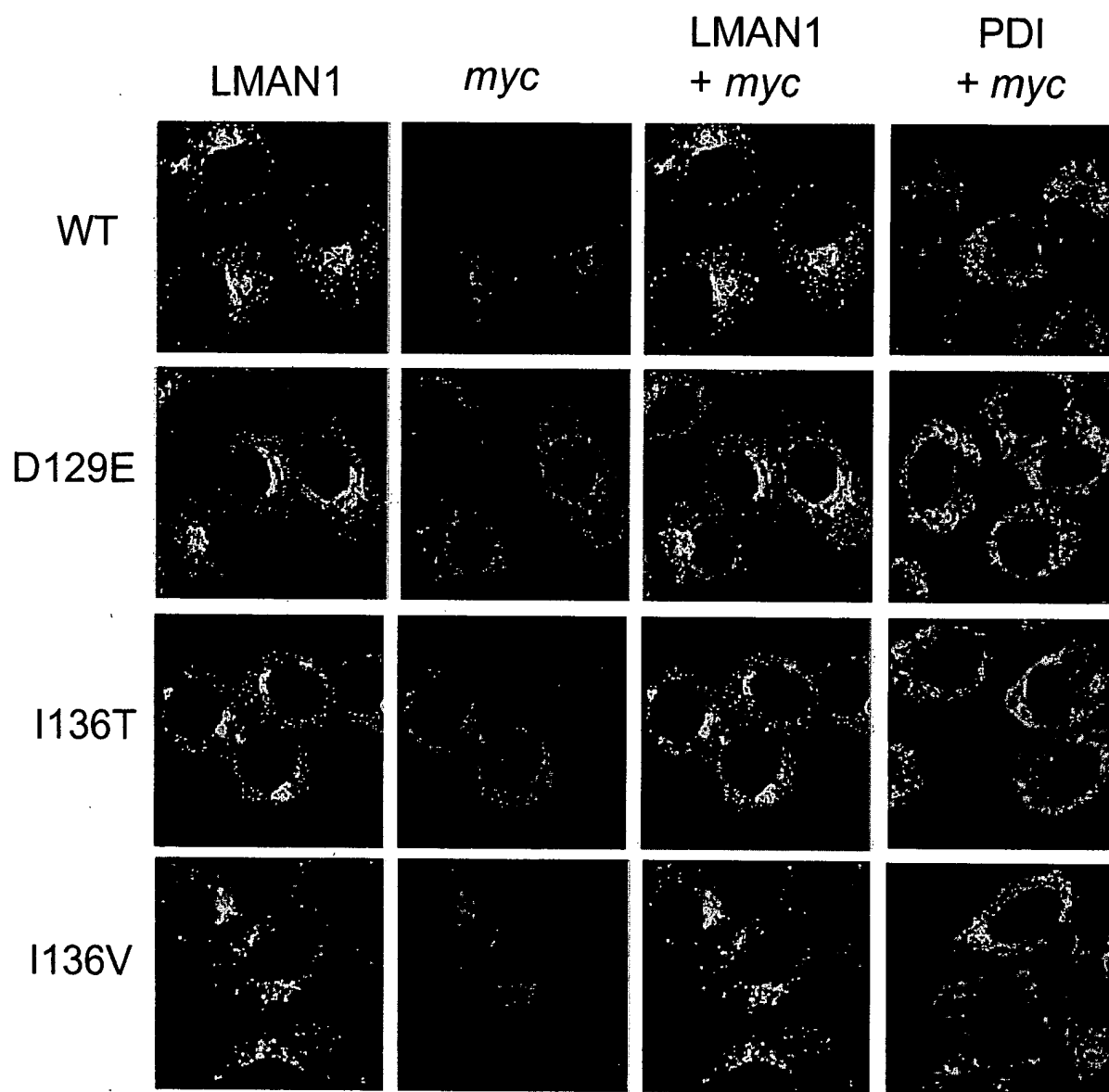
BEST AVAILABLE COPY

A

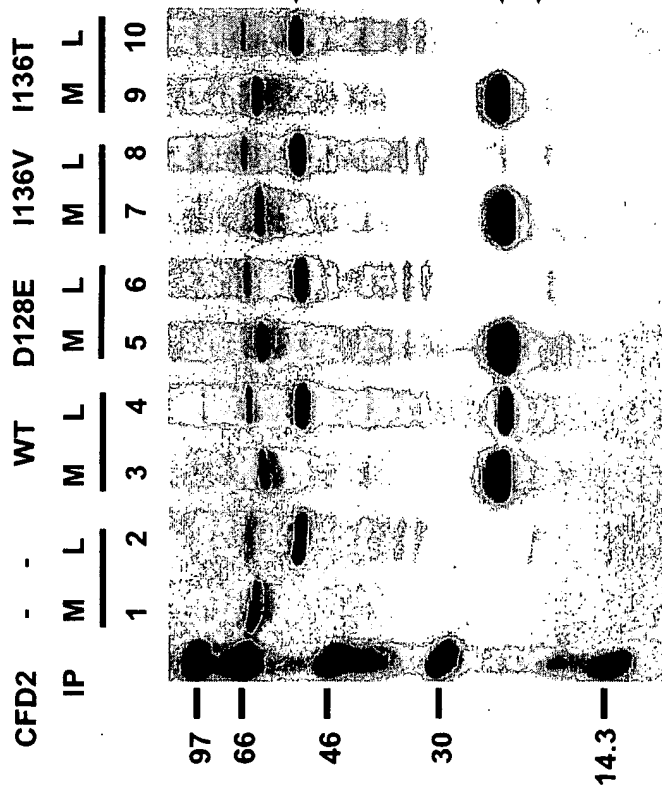


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FIG 5



A



B

CFD2 - - WT WT

Ca - - - - + +

EGTA - - - - + -

IP M L M L M L M L

1 2 3 4 5 6 7 8

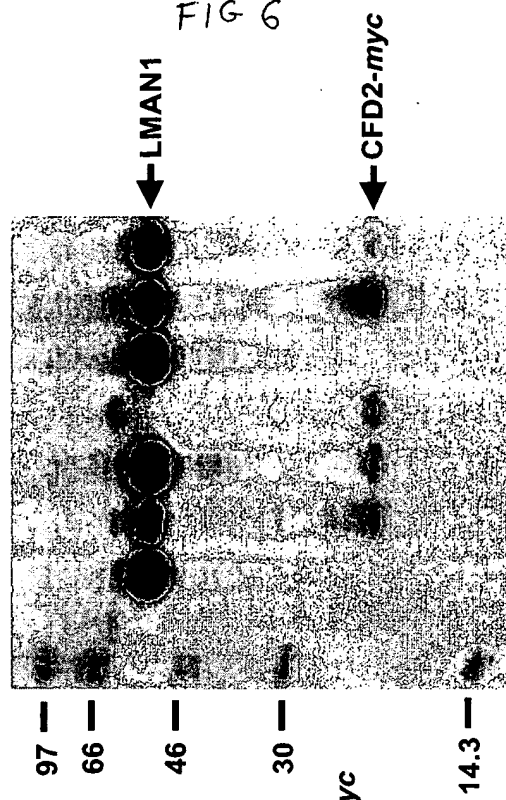


FIGURE 7

Full-length cDNA/mRNA (gene)

GGGCGAAGCCGAGGAAGAGCGTTTTTGGGGACGGGGGCTGGTGAGGCTCACGTTGGAGGGCTTCGCGTCTGC
TTCGGAGACCGTAAGGATATTGATGACCATGAGATCCCTGCTCAGAACCCCTTCTGTGTGGCCTGCTCT
GGGCCTTTTGTGCCCCAGGCGCAGGGCTGAGGAGCCTGCAGCCAGCTTCTCCCAACCCGGCAGCATGGGC
CTGGATAAGAACACAGTGCACGACCAAGAGCATATCATGGAGCATCTAGAAGGTGTCATCAACAAACCAGA
GGCGGAGATGTGCGCCACAAGAATTGCAGCTCCATTACTTCAAAATGCATGATTATGATGGCAATAATTTGC
TTGATGGCTTAGAACTCTCCACAGCCATCACTCATGTCCATAAGGAGGAAGGGAGTGAACAGGCACCACTA
ATGAGTGAAGATGAACTGATTAAACATAATAGATGGTGTTTTGAGAGATGATGACAAGAACAATGATGGATA
CATTGACTATGCTGAATTTGCAAAATCACTGCAGTAGATGTTATTTGGCCATCTCCTGGTTATATACAAAT
GTGACCCGTGATAATGTGATTGAACACTTTAGTAATGCAAAATAACTCATTTCCTCACTACTGCTGCAGCAT
TTTGGTAAAAACCTGTAGCGATTTCGTTACACTGGGGTGAGAAGAGATAAGAGAAAATGAAAAGAGAAGAGAAA
TGGGACATCTAATAGTCCCTAAGTGCTATTAAATACCTTATTGGACAAGGGCTTGCTTCAAGCATCTGTAT
TAGTCTGTATTAAATGCTGCTGATAAAGACGTACCCGAGACTGGGAAGAAAAAGAGGTTTACTTGGACTTAC
AGTTCCACATGGCTGGGGAGGCCTCAGAATCATGGCGGGAGGTGAAAGGCACTTCTTACATGGCAGCAAGA
GAAAATGAGGAAGAAGCAAAAGTGGAACCCCTGATAAGCCATCAGATCTTGTGAACTTATTCACTATCA
CAAGAATAGCATGGGAAGACTGGCCCCCATGATTCAATTACCTCCCTTGGGTCTCTCCACAACACGTG
GGAATTTCTGGTAGATAACAATTTCAAGTTGAGATTTGGGTGGGGACATAGCCAAACCATATCATTTTACCCC
TGGCCCTCCAAATCTCATGTCTCTACTATTTCAAAACCAATCATGCCTTCCCTAACAGTCCCCCAAGTCTT
AACTCTTTTTCAGCATTAACGCAAAAATCCACAGTCCAAAGTCTCATCTGAGACAAGGCAAGTCCCTTCAC
CTATGAGCCTGTAAATCAAAAAGCAAGCTAGTTACTTCCCTAGATACCAACAGGGGTACAGGTATTGATTAA
AGACGGCTGTTCCAAATGGGAGAAAATTGGCCAAAATAAAGGGGTACAGGGCCCATGCAAGTCCGAAATCC
AGCAGGGCTGTCAAATTTTAAAGTTCCAGAATAATCTCCTTTGACTCCAGGTCTCACATCCAGGTCATACT
GATGCAAGAAGTGGGTTCCCATGGTCTTGGGCAGCTCTGCCCTGTGGCTTTGTAGGGTACAGCCTCCCTC
CTGGCTGCTTTTACGGCTGTTGTTTCAGTGCTGCGGCTTTTCCAGGTGCACGGTGCAGCTGTTGGTGGAT
CTACCATTCTGGGGTCTGGAGGACGGTGGCCCTCTTCTCACAGCTCCACTAGGCAGTGCCCCAGTAGGGAC
TCTGTGTGGGGGCTCCACACCACATTTCCCTTCTGCACTGCCCTAGCAGAGGTTCTCTCCCTGCCGCTG
AGAGGGCTCTCCCTGTCAGCAACGTTTGCTGGGCATTGAGGCATTTCCATACATCTTCTGAAAAGTAG
GCGGAGGTTTTCCAAATCTCAATTTCTGACTTCTGTGCACCTGCAGGCTTAACAGCACATAGAAGCTGCCAA
GGCTTGGGGCTTCCACTCTGAAGCCACAGCCCCGAGCTGTATGTTGGCCCCCTTTCAGCCATGGCTGGAGTGG
CTGGGACACAAGACACCAAGTCCCTAGGCTGCACACACATGTGAGGGGCTGCCCTGACATGGCCTGGAGAC
ATTTTCCCCATGGTGTGTTGGGGATTAACTTAGGCTCCTTGCTACTTATGCAAATTTCTGCAGCTGGCTTGA
ATTTCTCCCCAGAAAATGGGTTTTTCTTTCTATTGCAATGTCAGGCTGCAAATTTCCAACTTTTATGCT
TTGCTTCCCTTATTATTAAGGAATGCCTTTAAAAGCACCCAAGTACCTGTTGAACACTTTGCTGCTTAG
AAATTTCTTCCGCTAGTTAACTAAATCATCTCTCTCAAGTTCAAAGTTCCACAAATCCCTATGGAAGGGG
CAAAATGCTGCCAGTCTCTTTGCTAAACATAACAAGACTACCTTTACTCCAGTTCCCAAACTGTTCTC
ATCTTCATCTGAGGCCACCTCAGCCTGGACTTTGTGTGTCATATTGCTATCAGCATTTGGGGCAAGGCCAT
TCAACAAGTCTGTAGGAAGTTCCAAACTTTCCACATTTTCTGTTTTCTTCTGAGCCCTCCAAACTGTTTC
CAGCCTCTGCCTGTTACCCAGTTCCAAAGTCACTTCCACATTTTGGGTATTTCTTCAGCAGGTCCCAATCT
ACTGGTACCAATTTACTGTATTAGTCCGTTTTTACGCTGCTGATAAAGACATAACCCGAGACTGGGAAGAAA
AAGTGGTTTTAATTGGACTTAAAGTTCCACATGGCTGGGGAGGCCTCAGAATCATGGTGGGAGGCAAAAGAC
ACTTCTTACATTGTGGCAAGAAAAAATGAGGAAGAAGCAAAAGCAGAAACCCCTGATAAACTGATCAGATC
TCATGAGACTTATTCACTGTCACGAGAATAGCACGGGAAAGACTGGCCCCATGATTCAATTACCTCCCC
TGGGTCTGTCCCAACACAGTGGGAATTCTGGGAGATACAATTCAAGTTGAGATTGTGGGGGACACAAC
CAACCATATCAGCATCCTTTCAAGAATATTAGATAATTGGAGCTGAGTACTCAGGAAGTTGACTGTAGTA
GAATACTGCTAGTTTCTTAATTTTAATTCACATACCTGAAAAGTAAAACAACAGGCTTTGCCAAGTGGAT
GCTTTTTCAGTAACAGTGAAGTGGAGTGAATACCAATGTTTGCCCTGGTGGTTTCTATCTCTTCAGGCAAA
CATGGTCAGTATTCTGTAAAGTTCCCTTGCCCTAAATGATTACTTGTCTGTTGGCAAGTGGATATTTATTAG
GCTATTTCAAAGCCACAGCATAAGAATGTCAGCCTAGCCACAGAGTCTGAGATTCTGAGTTTCAGCCTAGCC
ACAGAGTCTAAGATTCTGTATCCTCTGACATTTTGGAAATGATACACTACTGGCTTAAGTGATGACTCTTT
CAGATTTTTCAGTATTTTATACAATACTGCCACATCCTTATACTTTATTGCTTTTCTGTCTTCTTCAACCT
GGGAGAGACCCCTGAATTTGAGTGTGTTCTCTAATCAATAGTGGTTTAGCTTTCTTTTCTATTTCACTCGTT
TCTAGGGTTTTTTATTTGCAGTTTAGGAACTATTAGGAATGTCAGGACTTTATCAGCAGGGGTAAAAGTAC
CACCTGGCCTAGCCTAAGTAGGAAGTGAAGAGATAATTCACCAACAATGATTAATCAGATAGAAGTTCTA

GTCAAGAGGGATATTGTTGAAGTTACCTCTTTTAGCCTAGATACATGGATTCTTTTCAAATCAGGAAAGAT
TAGAAAAGGAACCCAAAAAACCTTTAACAGTGTGAATCTTTATAGTATTTGAAAAATGAGAAGAAGCAGCA
GATTGTAATTTGGTTTATTGGATGTGATGGACGTTCTGTAATAGAAAAACCTGAAACGATGATTGAATGGGA
AAAAGAGACTACAAAATTTGTCGTAGGATGTATACAGACTTATTTTCTTTATTACAGTATTATAAGAAAAC
ATATGTATTTGTAAAAATGGTTTCCTGTGTCAAGTATTTGTGCAGTCAGAGCTGACTTGTAACCTATTCTT
GTAATAGCTCATTATTTTGAAAGATTTATATATGATGAATTCTGGATATATGACCAATAAAACTGATGAAG
C

FIGURE 8

Amino Acid sequence (protein)

MTMRSLLRTPFLCGLLWAFCAPGARAEPAASFSPGSMGLDKNTVHDQEHIMEHLEGVINK
PEAEMSPQELQLHYFKMHDYDGNLLDGLELSTAITHVHKEEGSEQAPLMSEDELINIIDGV
LRDDDKNNDGYIDYAEFAKSLQ

FIGURE 9

Full-length cDNA with translation

GGGCGAAGCCGAGGAAGAGCGTTTGGGGACGGGGCTGGTGAGGCTCACGTTGGAGGGCTTCGCGTCTGC
 TTCGGAGACCGTAAGGATATTGATGACCATGAGATCCCTGCTCAGAACCCCTTCCTGTGTGGCCTGCTCT
 M T M R S L L R T P F L C G L L
 GGGCCTTTTGTGCCCCAGGCGCCAGGGCTGAGGAGCCTGCAGCCAGCTTCTCCCAACCCGGCAGCATGGGC
 W A F C A P G A R A E E P A A S F S Q P G S M G
 CTGGATAAGAACACAGTGCACGACCAAGAGCATATCATGGAGCATCTAGAAGGTGTCATCAACAAACCAGA
 L D K N T V H D Q E H I M E H L E G V I N K P E
 GGCGGAGATGTCGCCACAAGAAATTGCAGCTCCATTACTTCAAAATGCATGATTATGATGGCAATAATTTGC
 A E M S P Q E L Q L H Y F K M H D Y D G N N L
 TTGATGGCTTAGAACTCTCCACAGCCATCACTCATGTCCATAAGGAGGAAGGGAGTGAACAGGCACCCTA
 L D G L E L S T A I T H V H K E E G S E Q A P L
 ATGAGTGAAGATGAACGATTAAACATAATAGATGGTGTTTTGGAGAGATGATGACAAGAACAATGATGGATA
 M S E D E L I N I I D G V L R D D D K N N D G Y
 CATTGACTATGCTGAATTTGCAAAATCACTGCAGTAGATGTTATTTGGCCATCTCCTGGTTATATACAAAT
 I D Y A E F A K S L Q
 GTGACCCGTGATAATGTGATTGAACACTTTTAGTAATGCAAAATAACTCATTTCCAACCTACTGCTGCAGCAT
 TTTGGTAAAAACCTGTAGCGATTCTGTTACACTGGGGTGAGAAGAGATAAGAGAAATGAAAGAGAAGAGAAA
 TGGGACATCTAATAGTCCCTAAGTGCTATTAAATACCTTATTTGGACAAGGGCTTGCTTCAAGCATCTGTAT
 TAGTCTGTATTAAATGCTGCTGATAAAGACGTACCCGAGACTGGGAAGAAAAAGAGGTTTACTTGGACTTAC
 AGTTCCACATGGCTGGGGAGGCCCTCAGAATCATGGCGGGAGGTGAAAGGCACCTTCTTACATGGCAGCAAGA
 GAAAATGAGGAAGAAGCAAAAGTGGAACCCCTGATAAGCCATCAGATCTTGTGAAACTTATTCACATATCA
 CAAGAATAGCATGGGAAAGACTGGCCCCCATGATTCAATTACCTCCCCTTGGGTCTCTCCCAACACAGTG
 GGAATTCTGGTAGATAACAATTTCAAGTTGAGATTTGGGTGGGGACATAGCCAAACCATATCATTCTACCCC
 TGGCCCCCTCCAAATCTCATGTCTCTCACTATTCAAAACCAATCATGCCTTCCCTAACAGTCCCCCAAAGTCTT
 AACTCTTTTCAGCATTAACGCAAAAATCCACAGTCCAAAGTCTCATCTGAGACAAGGCAAGTCCCCTCCAC
 CTATGAGCCTGTAAAATCAAAAGCAAGCTAGTTACTTCTCTAGATACCAACAGGGGTACAGGTATTGATTAA
 AGACGGCTGTTCCAAATGGGAGAAATTTGGCCAAAATAAAGGGGTACAGGGCCCATGCAAGTCCGAAATCC
 AGCAGGGCTGTCAAATTTTAAAGTTCCAGAATAATCTCCTTTGACTCCAGGTCTCACATCCAGGTCTACT
 GATGCAAGAAGTGGGTTCCTCATGGTCTTGGGCAGCTCTGCCCCCTGTGGCTTTGTAGGGTACAGCCTCCCTC
 CTGGCTGCTTTTACGGCTGTGTTTCACTGCTTGGCGCTTTTCCAGGTGCACGGTGCAGCTGTTGGTGGAT
 CTACCATCTGCGGTCTGGAGGACGGTGGCCCTTCTCTCACAGCTCCACTAGGCAGTGCCTCCAGTGGGAC
 TCTGTGTGGGGCTCCCAACACCATTTCCCTTCTGCATGCCCCTAGCAGAGGTCTCTCCCTGCGCGTG
 AGAGGGCTCTCCCTGCGCAAAACGTTTGCCTGGGCATTGAGGCATTTCCATACATCTTCTGAAAACCTAG
 GCGGAGGTTTCCAAATCTCAATTTCTGACTTCTGTGCACCTGCAGGCTTAACAGCACATAGAAGCTGCCAA
 GGCTTGGGGCTTCCACTCTGAAGCCACAGCCGAGCTGTATGTTGGCCCCCTTTCAGCCATGGCTGGAGTGG
 CTGGGACACAAGACACCAAGTCCCTAGGCTGCACACACATGTCAGGGGCTGCCCTGACATGGCTGGAGAC
 ATTTTCCCCATGGTGTGGGGATTAACATTAGGCTCCTTGCTACTTATGCAAATTTCTGCAGCTGGCTTGA
 ATTTCTCCCCAGAAAATGGGTTTTTCTTTTCTATTGCATAGTCAGGCTGCAAATTTCCAAACTTTTATGCT
 TTGCTTCCCTTATTTATAAGGGAATGCCTTTAAAGCACCCAAGTCACCTGTTGAACACTTTGCTGCTTAG
 AAATTTCTTCCGCCAGTTAACCATAATCATCTCTCTCAAGTTCAAAGTTCCACAAATCCCTATGGAAGGGG
 CAAAATGCTGCCAGTCTCTTTGCTAAAACATAACAAGAGTCACCTTTACTCCAGTTCCCAACAAGTTCCCTC
 ATCTTCATCTGAGGCCACCTCAGCCTGGACTTTGTTGTCCATATTGCTATCAGCATTTGGGGCAAAGCCAT
 TCAACAAGTCTGTAGGAAGTTCCAAACTTTCCACATTTTCCCTGTTTTCTTCTGAGCCCTCCAAACTGTTT
 CAGCCTCTGCCTGTTACCCAGTTCCAAAGTCACTTCCACATTTTGGGTATTTCTTCAGCAGGTCCCAATCT
 ACTGGTACCAATTTACTGTATTAGTCCGTTTTTACGCTGCTGATAAAGACATACCCGAGACTGGGAAGAAA
 AAGTGGTTTAAATTGGACTTAAAGTTCCACATGGCTGGGGAGGCCTCAGAATCATGGTGGGAGGCAAAAGAC
 ACTTCTTACATTGTGGCAAGAAAAAATGAGGAAGAAGCAAAAGCAGAAACCCCTGATAAACTGATCAGATC
 TCATGAGACTTATTCATGTACGAGAATAGCACGGGAAGACTGGCCCCCATGATTCAATTACCTCCCCC
 TGGGTCTGTCCCAACACAGTGGGAATTCTGGGAGATAACAATTCAGTTGAGATTTGTGGGGGGACACAAC
 CAAACCATATCAGCATCCTTTCAAGAATATTAGATAATTGGAGCTGAGTACTCAGGAACCTTGACTGTAGTA
 GAATACTGCTAGTTTCTTAATTTTAAATTCACATCACCTGAAAAGTAAAACAACAGGCCTTTGCCAAGTGGAT
 GCTTTTCAGTAACAGTGAAGTGGAGTGAATACCAATGTTTGGCCCTGGTGGTTCCTATCTCTCAGGCAAA

CATGGTCAGTATTCTGTAAAGTTCCCCTGGCCTAAATGATTACTTGCTCTGGGCAAGTGGATATTTATTAG
GCTATTTCAAAGCCACAGCATAAGAATGTCAGCCTAGCCACAGAGTCTGAGATTCTGAGTTCAGCCTAGCC
ACAGAGTCTAAGATTCTGTATCCTCTGACATTTTGGAAATGATACACTACTGGCTTAAGTGATGACTCTTT
CAGATTTTCAGTATTTTATACAACACTACTGCCACATCCTTATACTTTATTGCTTTTCTGTCTTCTTCAACCT
GGGAGAGACCCTGAATTTGAGTGTGTTCTCTAATCAATAGTGGTTTAGCTTTCTTTTCTATTTCACTCGTT
TCTAGGGTTTTTTTATTTGCAGTTTAGGAACTATTAGGAATGTCAGGACTTTATCAGCAGGGGTAAACTAC
CACCTGGCCTAGCCTAAGTAGGAAGTGAAAAGATAATTCACCAACAATGATTAATCAGATAGAAGTTCTA
GTCAAGAGGGATATTGTTGAAGTTACCTCTTTTAGCCTAGATACATGGATTCTTTTCAAATCAGGAAAGAT
TAGAAAAGGAACCCAAAAAACCTTTAACAGTGTGAATCTTTATAGTATTTGAAAATGAGAAGAAGCAGCA
GATTGTAATTTGGTTTATTGGATGTGATGGACGTTCTGTAATAGAAAACCTGAAACGATGATTGAATGGGA
AAAAGAGACTACAAAATTTGTCGTAGGATGTATACAGACTTATTTCTTTATTACAGTATTATAAGAAAAC
ATATGTATTTGTAAAAATGGTTTCCTGTGTCAAGTATTTGTGCAGTCAGAGCTGACTTGTAACCTATTCTT
GTAATAGCTCATTATTTTGAAAGATTATATATGATGAATTCTGGATATATGACCAATAAACTGATGAAG
CAAAA

FIGURE 10

Genomic sequence (exons are underlined)

```

1          11          21          31          41          51
AAGCAATACTAAAAGGTGTAATTTGAAATCTTATTTTCACCCCTATTCTCATCCACTCTG
61          71          81          91          101         111
GAATCCCCCTACATAGGTAAAACATTGTCTTGAGACAATTCAAAACAGCTGAGGAAAGAGA
121         131         141         151         161         171
TGCCACCTAGAGGCCATTCTGGTATCTTGGGATGGCCGTCCTATCTCCTGATAAAGCCAC
181         191         201         211         221         231
CTCTCTGTCTCTACTTGTACTAGTTTCAACCTGAGTACACAAAGTAAATGGGGTATTTCA
241         251         261         271         281         291
GCAAGGTTCCAAGTTATGAGACTCCTGGTTGCAGGTAAAGAGATCCTCTCTTACCTAGTC
301         311         321         331         341         351
GTTACTTTCTTTAATCTCTGCTTTCAAATCAGTTATTTCCAACGTAGAGTTGCCCTTCTC
361         371         381         391         401         411
TTGAAGGAGTCTGCTGAAAAGCTACTAAAAAAGGCAACACTCACTAATGTTCCATATTGCT
421         431         441         451         461         471
CGTGAGATTTCTCCAAAAATATAGCATTGGTTGGCATGTGGCCTATATCCAAGGTCCAGC
481         491         501         511         521         531
AAGTGACAGTTTCACTACGGCTTATAAGGGTCACCAACTTTCCAGTTTGACATACAGTCT
541         551         561         571         581         591
TTTAACACTGGCTACCTTAACCTCCAGTTAGCCAATTCATATTTTAGTGTCTTGTTTTTT
601         611         621         631         641         651
AGCATCCTGCTTCTGGTACCAAATTATTTGCCTGTTAGGAATGGGTTCAGCTACAAGTTA
661         671         681         691         701         711
CAGAACACCCACCTATAAAATGGCTTAATCAAAGGTGGCTTCTCACTTATGGACTACAGT
721         731         741         751         761         771
AGGGCAAGAATGGAAGCAGGACGGTCAGTTAGGAAGCTCTCTCTCAAGTAGTCCAGCAGC
781         791         801         811         821         831
ATCATCTACTACTGGACTAGATGGTTTAGTGGAGGTGAAAAGAAGTCAAAGACTCAGGAT
841         851         861         871         881         891
ACATTTTGTATAGCATCAACAGGCTTTGCTGAAGGATTTAAAGGTAAAGGGATGAGATAAA
901         911         921         931         941         951
TCAAAAACAGCTCGTAGAATTTTAGCTTGAACAACAGAATGAGTACCAGTGACATTTACT
961         971         981         991         1001        1011
AAAATGCACAAGACTGAGAGAGGTGCAGGTTTGGGGGTGAAAATCAAGATTTTGGGGGGA
1021        1031        1041        1051        1061        1071
CACATTAAGTTTGAGATGCCAGTCTGACATTCATATGGAGACATCAAGTAGGCAGTTATT
1081        1091        1101        1111        1121        1131
TACAGGAGCCAGGAATTACACAGAGAGGTCATTGTCAGAGAGACATATTTTGGAGTCATC
1141        1151        1161        1171        1181        1191
TATTTATAAATGGTATCTAAAGCACAGGACTAGGTAAACTCACATAGGGAGGGTGGATAG
1201        1211        1221        1231        1241        1251
AGAAGGTGACTCAGAACAGAACCCCTGGACACTTTGATAATTATAGATTGAGAAGCCAATT
1261        1271        1281        1291        1301        1311
AAGAAGCCCAAGAAAGGATAATGAGTGAGGTAGCAGAAGGACCCAGAGTGTGTGGTGTCA
1321        1331        1341        1351        1361        1371
GAAAACAAGAGAAGAAAGTGTCTAAGTGAGAGTGGTTGGCTTTGATAAAACAGTGTTG
1381        1391        1401        1411        1421        1431
AGAGGGCAAGTAAAAATAAAAACAAGAGATCAAAGAGACCACCTAGATTTGCATGGAGATTG
1441        1451        1461        1471        1481        1491
CAGTTTTCAGTGGTATGGTGGGGGAGAAAATACAGCAAGTTTATATGTTGATGGGAATTAT
1501        1511        1521        1531        1541        1551
CTGGTAGAGAGGGAGTGACTGTAGATTCAAGAGAGACATAACACAGGATAACATCCATAG

```

1561	1571	1581	1591	1601	1611
GAAAAAAATGAAAGCACTGGCTAGAATGAGGACACTTTATCCATCTACCAGACACCAGCT					
1621	1631	1641	1651	1661	1671
TCTTGACACTTCATTTGTCTTATTTGTATCTCTAGTAGCTCCTAGTAGAGCGCCTAGTAC					
1681	1691	1701	1711	1721	1731
ATAGAAGATATTCAAGAAATGTTATTGAATGAATAAATGAACAAAGGGAGGGGTGGATGA					
1741	1751	1761	1771	1781	1791
ATGGATGAAGAGATGGATGAATGGCAGATGCAGGGTAGAAGGAGGAACTAGATCAAACCTA					
1801	1811	1821	1831	1841	1851
ATCCAAAGTTCAGAGTAAGGAAAGAAGAATGGGTCTTGAATTAATAGGGTTTCCTCAAAA					
1861	1871	1881	1891	1901	1911
CTTAGGGATTCTTTGTCCCGCGCGGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGG					
1921	1931	1941	1951	1961	1971
CGGAGGTGGTGGGAGGATTGCTTGAACCCAGGAGTTCGAGACGAGCTGGGCACCATGGAG					
1981	1991	2001	2011	2021	2031
ACTCTTTTCTTTAAAAAAGAAAAAAATTAGGGATTATGGGATTTTCTCTGGGATGG					
2041	2051	2061	2071	2081	2091
GGTGGCAGATTTCAATCTCAGATGAAGGTGGGAAAAGGAATGAGACCGTCAATGGCAGTG					
2101	2111	2121	2131	2141	2151
GCGTTAGGCAACTTTCAAGGCATCTAACTACTTAGCCACTTTCTTTGTCTTTCTGTCCG					
2161	2171	2181	2191	2201	2211
GACCCAGGCTCATTTGAAAAACGATTATGTACCTTTATGGACAGAAATGGGAGAAGGGCT					
2221	2231	2241	2251	2261	2271
TTAAAAAAACGACCGTCCTGCCGGGAGTGGTGGCTCACGCCTGTAATCCCAGCACTTTG					
2281	2291	2301	2311	2321	2331
GGAGGCTGAGGCGGGAGGATCAAGAGGTCAGCAGTTAGAGACCAGCCTGGCCAACACGGT					
2341	2351	2361	2371	2381	2391
GAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGGCAAGGTGGCACGCGCCTGTAA					
2401	2411	2421	2431	2441	2451
TCCCAGCTACTCGGGAGGCTGAGGTAGGAGAAGAGCTTGAACCTGGGAGGCGGAGGTTGC					
2461	2471	2481	2491	2501	2511
AGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGGACAGAGCGAGACTCCGTCTCAAA					
2521	2531	2541	2551	2561	2571
ACAAAACAAAACAAAACAAAACAAAACGACCGTCCTACACTCATTTATCCATCAGGT					
2581	2591	2601	2611	2621	2631
CAATGGATACTTACTGAATGTTAATCTTGTATAGGAGCACAGGTGTAAGGGCAGGATTAT					
2641	2651	2661	2671	2681	2691
ACAGGGATGAATTCGATACAGGGATGATGTATTTCGTTTCCCTATTTGTTTCATGAGTCTGT					
2701	2711	2721	2731	2741	2751
TTTTAAGTAATCTGTCTCTCTTGAATGTCAAAAGCTGCTGATTTACGAACGGTACATG					
2761	2771	2781	2791	2801	2811
GAAGATGGTATTTGAACTGGGTGCGATAGTCTTGCTGGGACTCCCGTGAAGCGAACGGG					
2821	2831	2841	2851	2861	2871
GACAGCGGCTGCCGAGCTTGTGCAGTGGAGCTGGCAGACGCTGGAAGCAGGCCAATCTT					
2881	2891	2901	2911	2921	2931
GAAACGTAGGGTCCAAGGCCGGCTCCAGCGTGTGTGGTCGTTTCATCAAGAAGGAATTA					
2941	2951	2961	2971	2981	2991
GCATTCCCTATTATCTTTCTTCCCAACTTGCAGCAGGACGAACCAAGAGACCTGAACCAAG					
3001	3011	3021	3031	3041	3051
AGCCCTGTATAGGAGGGGGTGAGCGGAGTTGGGAGCCAGCTTTGGGGTCCGCCCCATCCG					
3061	3071	3081	3091	3101	3111
GATCCGCCATCTACGTCGCCCCGTGGAACCTACGTTCTGAGGGCTTCCGGCGTTGCCTAG					
3121	3131	3141	3151	3161	3171
CAACTGCCGGGCCCCCTAGGGCGTCCAGCGGCCCAACTGGAGTGGAGCCGAGTGTGCGCCCT					
3181	3191	3201	3211	3221	3231
TGGGAAAGCAGGTAGAAGAACTGCGTCAGTCCCGCCAGTGCTGGGCCCCGGGCCGATTACA					
3241	3251	3261	3271	3281	3291

CGTGGACTCACGCGAGCCGTCCTCACAGCCCCGCCGCCAGCGGGAGGGGCCCCGGCGGC
 3301 3311 3321 3331 3341 3351
 GCCAATGGGCGGCGGCAGGGAGCGCGCTCCGGGCAGGTTCGGGGGGGGGGGGGGGGGGCGGG
 3361 3371 3381 3391 3401 3411
 GCGAAGCCGAGGAAGAGCGTTTTGGGGACGGGGGGCTGGGTGAGGCTCACGTTGGAGGGCTT
 3421 3431 3441 3451 3461 3471
 CGCGTCTGCTTCGGAGACCGTAAGGGTGAGTGAAGTAGCGCACTCTCCGCAGCGGGCGGG
 3481 3491 3501 3511 3521 3531
 ATCCCGGCGCCTCTCTGTGGGCTGGAGGCTTGGGCTCAAGATGAGAGGCAGGAGTAGTC
 3541 3551 3561 3571 3581 3591
 TGGGGGCGCGGCTGGCCCCCAGGCCGTCTCGGGACGCTTAACCGGCTAGGAGCACGGCCT
 3601 3611 3621 3631 3641 3651
 GTCTCCCGGGCGGAAGCCTGTGTCCACCGGGGCTCTGGAGCCAGACGGGGCCGACTGGGC
 3661 3671 3681 3691 3701 3711
 AGATCTCCGCCCCCTTCCCTGGTCCCTAGGGGGCCGAGGATCGGCCTGTGGGACCAGCTG
 3721 3731 3741 3751 3761 3771
 TGTCGGGTGGACACTGCTCCTGGCCCCGGCCCAAAAGCAGCGGGCCGGAAGCCTTACTCTC
 3781 3791 3801 3811 3821 3831
 CCTCTGCTCCTTGTTCCTCTCTCGGGGAGACCACAGGTCCTGTGGGGCCGGCGGGGGA
 3841 3851 3861 3871 3881 3891
 AGCTGATCTCCTGTGTATTCCCTCTCTGGGCATGGCCATCCACCCGGGTGCCAAGCCA
 3901 3911 3921 3931 3941 3951
 GAATTGGGCATCATTCTCACTTGCTTCACTCCTTTACCCACCCACATCGAATCCCTTGCA
 3961 3971 3981 3991 4001 4011
 AAGTTGTCTTGGATACGTTTCATTCTCCAGTCCCATCCCCCTGCCCTACCTAGTTTCAGGCC
 4021 4031 4041 4051 4061 4071
 ACCTTTTCTTCTCTGGACTACCTCGGTGTCTTCTCTGATGATCCCTGCATCTCTTCTTCAT
 4081 4091 4101 4111 4121 4131
 CCTCTGTAGTTTGTCTTATACAGAGAGGCTACAGCCATGGTCTTAAACAGAAATCTGAT
 4141 4151 4161 4171 4181 4191
 CATGTGACCAGAAGCGTCCCCCATTCCTTATCACCTTTGGTGGATTCTCATTGCTCT
 4201 4211 4221 4231 4241 4251
 TCCAAGCTCTTGAACGGGGCTTGCAAAGCCCTTCATGACCTGTCTTCCCTTAACTTTAGA
 4261 4271 4281 4291 4301 4311
 TTCATTGTCTCGACTGTACTGTGTCTTCAACCATACTGAATCTTTTTTGGTTCTTAGAT
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8521	8531	8541	8551	8561	8571
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8581	8591	8601	8611	8621	8631
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8641	8651	8661	8671	8681	8691
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